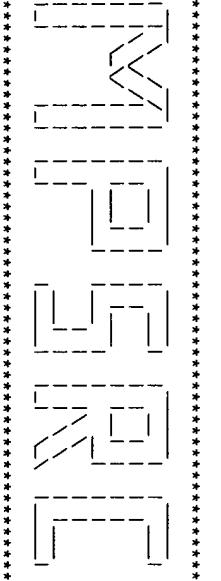


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Mpsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Sat May 13 08:59:53 2000; MasPar time 4.30 Seconds

Tabular output not generated.

Title: >US-09-331-631-24

Description: (31-85) from US0931631.pep

Perfect Score: 425

Sequence: 1 DEDDRGGHSLOQCVQRCRQ . . . . . DDQQQHIGRHEQQEEQGRG 55

Scoring table: PAM 150

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq35  
1.geneseqp

Statistics: Mean 23.878; Variance 101.499; scale 0.235

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query Length	DB ID	Description	Pred. No.
1	425	100.0	637	Hordeum vulgare antimi	2.03e-31
2	174	40.9	593	Zea mays antimicrobial	1.55e-07
3	131	30.8	590	1 W62835	Gossypium hirsutum ant
4	129	30.4	666	1 W62828	Macadamia integrifolia
5	129	30.4	666	1 W62829	Macadamia integrifolia
6	105	24.7	625	1 W62830	Macadamia integrifolia
7	105	24.7	898	1 W36853	Mycobacterium tuberculosis
8	95	22.4	409	1 W9042	G. max truncated SBP2
9	95	22.4	489	1 W90341	G. max truncated SBP2
10	89	20.9	525	1 W62831	Theobroma cacao antimi
11	89	20.9	565	1 W19764	Tyrosine kinase assoc
12	85	20.0	450	1 W46006	Human HER-2/neu oncoge
13	84	19.8	97	1 W59348	Human ErBB2 extracellular
14	84	19.8	444	1 W9340	G. max truncated SBP1
15	84	19.8	524	1 W90339	G. max SBP1 protein
16	84	19.8	624	1 W6222	Extacellular portion
17	84	19.8	782	1 W19764	HER-2/GM-CSF immunostim
18	84	19.8	1255	1 W92406	Human HER-2/neu oncoge
19	84	19.8	1255	1 W0111	HER-2/neu protein.
20	83	19.5	195	1 W2150	Peanut allergen Ara h1
21	83	19.5	1829	1 Y0742	Actin-filament binding
22	82	19.3	559	1 W3628	Yeast transcriptional
23	82	19.3	1 W97834	Human Fc receptor I.	

ALIGNMENTS					
RESULT	1	ID	W62837	standard; Protein;	637 AA.
Match		ID	W62837	27-OCT-1998 (first entry)	
Matches	55	AC		Hordeum vulgare antimicrobial protein.	
		DT		Hordeum vulgare antimicrobial protein; infestation; control.	
		KW		Hordeum vulgare.	
		OS			
		OS			
		PN			
		PD		W09827805-A1.	
		PF		02-JUL-1998.	
		PR		22-DEC-1997; AU0874.	
		PA		20-DEC-1996; AU-004275.	
		(RETR.) COOP RES CENT TROPICAL PLANT PATHOLOGY.			
		PT		Bower NI, Goultier KC, Green JL, Manners JM, Marcus JP;	
		DR		WPI: 98-37279/32.	
		PT		Novel anti-microbial protein from e.g. Macadamia integrifolia - useful for controlling microbial infestations of plants or mammals	
		CC		Claim 1; Page 60-62; 96pp; English.	
		CC		The sequence is that of an antimicrobial protein which can be used to control microbial infestations in plants and mammalian	
		CC		animals.	
		SQ		Sequence 637 AA;	
		Query		100.0%; score 425; DB 1; Length 637;	
		Match		Best Local Similarity 100.0%; pred. No. 2.03e-31;	
		Matches		Mismatches 0; Indels 0; Gaps 0;	
		Db	31	DEDDRGGHSLOQCVQRCRPVRSHARWQECDDQOHGRHQEEQGRG 85	
		Ov	31	DEDDRRGGHSLOQCVQRCRPVRSHARWQECDDQOHGRHQEEQGRG 85	
		RESULT	2		
		ID	W62835	standard; Protein; 593 AA.	
		AC	W62835;		
		DT	R22835;		
		DE	27-OCT-1998 (first entry)		
		KW	Zea mays antimicrobial protein.		
		OS	antimicrobial protein; infestation; control.		
		PN	W09827805-A1.		
		PD	02-JUL-1998.		
		PF	22-DEC-1997; AU0874.		
		PR	20-DEC-1996; AU-004275.		
		PA	(RETR.) COOP RES CENT TROPICAL PLANT PATHOLOGY.		
		PT	Bower NI, Goultier KC, Green JL, Manners JM, Marcus JP;		
		DR	WPI: 98-37279/32.		
		PT	Novel anti-microbial protein from e.g. Macadamia integrifolia - useful for controlling microbial infestations of plants or mammals		

PS Claim 1; Page 58-60; 96pp; English.  
 CC The sequence is that of an antimicrobial protein which can  
 CC be used to control microbial infestations in plants and mammalian  
 animals.  
 Sequence 593 AA;

Query Match 40.9%; Score 174; DB 1; Length 593;  
 Best Local Similarity 32.7%; Pred. No. 1.55e-07;  
 Matches 18; Conservative 22; Mismatches 13; Indels 2; Gaps 2;

Db 27 DNHHHGHSQCVYRC-EDRPHWQRPRLEQREERERK-ROERSHADRS 79  
 QY 31 DEDERRGGHSLQQCVQRCRQEPYSHARCVQECRQDDQOOGHRHQEEQGRG 85

RESULT 3  
 ID W62832 standard; Protein: 590 AA.  
 AC W62832;  
 DT 27-OCT-1998 (first entry)  
 DE Gossypium hirsutum antimicrobial protein.  
 KW antimicrobial protein; infestation; control.  
 OS Gossypium hirsutum.  
 PN W09827805-A1.  
 PD 02-JUL-1998.  
 PF 22-DEC-1997; AU0874.  
 PR 20-DEC-1996; AU-004275.  
 PA (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.  
 PI Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;  
 DR WPI: 98-37279/32.  
 PT Novel anti-microbial protein from e.g. Macadamia integrifolia -  
 Useful for controlling microbial infestations of plants or mammals  
 PS Claim 1; Page 49-51; 96pp; English.  
 CC The sequence is that of an antimicrobial protein which can  
 be used to control microbial infestations in plants and mammalian  
 animals.  
 Sequence 590 AA;

Query Match 30.8%; Score 131; DB 1; Length 590;  
 Best Local Similarity 26.9%; Pred. No. 1.08e-03;  
 Matches 14; Conservative 23; Mismatches 14; Indels 1; Gaps 1;

Db 114 EEQEQQSQRQFOEQCQHQCHQEQRRBKKQCVRCREKQENPARGEREEA 165  
 QY 31 DEDERRGGHSLQQCVQRCRQEPYSHARCVQECRQDDQOOGHRHQEEQGRG 81

RESULT 4  
 ID W62828 standard; Protein: 666 AA.  
 AC W62828;  
 DT 27-OCT-1998 (first entry)  
 DE Macadamia integrifolia antimicrobial protein.  
 KW antimicrobial protein; infestation; control.  
 OS Macadamia integrifolia.  
 FH Key Location/Qualifiers  
 FT Peptide 1..28  
 /note= "signal peptide"  
 FT Protein 29..666  
 /note= "mature protein"  
 PN W09827805-A1.  
 PD 02-JUL-1998.  
 PF 22-DEC-1997; AU0874.  
 PR 20-DEC-1996; AU-004275.  
 PA (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.  
 PI Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;  
 DR N-PSDB; V42310.  
 Novel anti-microbial protein from e.g. Macadamia integrifolia -  
 useful for controlling microbial infestations of plants or mammals  
 PS Claim 1; Page 34-36; 96pp; English.  
 CC The sequence is that of an antimicrobial protein which can  
 be used to control microbial infestations in plants and mammalian  
 animals.  
 Sequence 666 AA;

RESULT 5  
 ID W62829 standard; Protein: 666 AA.  
 AC W62829;  
 DT 27-OCT-1998 (first entry)  
 DE Macadamia integrifolia antimicrobial protein.  
 KW antimicrobial protein; infestation; control.  
 OS Macadamia integrifolia.  
 FH Key Location/Qualifiers  
 FT Peptide 1..28  
 /note= "signal peptide"  
 FT Protein 29..666  
 /note= "mature protein"  
 PN W09827805-A1.  
 PD 02-JUL-1998.  
 PF 22-DEC-1997; AU0874.  
 PR 20-DEC-1996; AU-004275.  
 PA (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.  
 PI Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;  
 DR N-PSDB; V42316.  
 Novel anti-microbial protein from e.g. Macadamia integrifolia -  
 useful for controlling microbial infestations of plants or mammals  
 PS Claim 1; Page 43-45; 96pp; English.  
 CC The sequence is that of an antimicrobial protein which can  
 be used to control microbial infestations in plants and mammalian  
 animals.

Sequence	625 AA;
Query Match	24.7%; Score 105; DB 1; Length 625;
Best Local Similarity	31.1%; Pred. No. 1.83e-01;
Matches	14; Conservative 16; Mismatches 12; Indels 3; Gaps 2;
ID	141 EGDNNKDRPQQREYEDCRHRHCEQEPRL-QYQCCRQCOEQORHGR 184
AC	: 1::1 : ::1 : 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1:
DT	27-APR-1998 (first entry)
PT	Mycobacterium tuberculosis 77 kDa protein.
KW	tuberculosis; mycobacteria; infection; diagnosis;
CC	anti-mycobacterial; antibiotic; vaccine.
OS	Mycobacterium tuberculosis.
DR	W09741152-A2.
PN	06-NOV-1997.
PF	18-APR-1997; E01973.
PR	29-APR-1996; DE-017184.
PA	(GBFRB) GBF GES BIOTEC FORSCHUNG GMBH.
PI	Espitia C, Honisch C, Moreno C, Singh M;
CC	WPI; 97-54975050.
DR	N-PSD8; T93610.
PT	New DNA and related proteins or RNA derived from <i>M. tuberculosis</i> - used for diagnosis of mycobacterial infections, monitoring vaccination and development of anti-mycobacterial agents
PS	Claim 7; Fig 14; 55pp; English.
CC	This novel 77 kDa protein is encoded by an open reading frame of a Mycobacterium tuberculosis DNA fragment (see T93610) containing polymorphic GC-rich sequences. It is highly enriched in glycine and may be a cell wall protein. Novel <i>M. tuberculosis</i> proteins (see WO971851-57) are claimed. These can be produced as recombinant proteins, especially in bacterial, yeast, fungal or higher eukaryotic host cells, and used for diagnosing tuberculosis and other mycobacterial infections in humans or animals. The claimed proteins can also be used for epidemiological studies, for monitoring vaccination, and for the development of vaccines and anti-mycobacterial drugs.
SQ	Sequence 898 AA;
Query Match	22.4%; Score 95; DB 1; Length 409;
Best Local Similarity	36.2%; Pred. No. 1.24e+00;
Matches	17; Conservative 11; Mismatches 13; Indels 6; Gaps 5;
ID	W90341 standard; protein; 489 AA.
AC	W90341;
DT	24-MAY-1999 (first entry)
DE	G. max SBP2 protein.
KW	SBP1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant; seed; carbohydrate content; soybean.
OS	Glycine max.
DR	W09850986-A1.
PN	26-NOV-1998.
PF	21-MAY-1998; U10465.
PR	(UNIW ) UNIV WASHINGTON STATE RES FOUND.
PA	PAI Chao WS, Grimes HD;
PI	WPI; 99-070155/06.
DR	New modified plant sucrose binding proteins - used to develop transgenic plants which can have enhanced or decreased sucrose uptake activity in developing seeds
PT	PT Claim 13b; Page 37-38; 58pp; English.
PS	This sequence represents a novel sucrose binding protein, SBP2 isolated from Glycine max. This protein is used in a method resulting in the production of a modified plant sucrose binding protein (SBP) which has a modified amino acid sequence compared to a corresponding wild-type SBP, and where expression of the modified SBP in a yeast assay system confers enhanced sucrose uptake compared to the corresponding wild-type SBP. The products of the invention can be used for producing transgenic plants which have modified sucrose uptake activity, particularly in developing seeds. Enhanced sucrose uptake activity in developing seeds may be desirable where it is an advantage to increase the carbohydrate content of the seed (e.g. where the seed is the primary plant material harvested, such as soybean). In contrast, decreased sucrose uptake activity in seeds might be desirable where the vegetative material of the plant is harvested. The SBP regulatory regions confer specific or enhanced expression in developing seeds and so may be used to express any transgene in developing seeds.
SQ	Sequence 489 AA;
Query Match	22.4%; Score 95; DB 1; Length 489;
Best Local Similarity	36.2%; Pred. No. 1.24e+00;
Matches	17; Conservative 11; Mismatches 13; Indels 6; Gaps 5;
ID	39 LYTCKKDQCDR-QYEDSKRCLQC-DSMK-E-PEKQVETEERK 82
AC	41 ILOOCVQRCPYRSHA-R-CVQBCRDQQGHRHEQEBOGR 84
DT	26-NOV-1998.
PT	New modified plant sucrose binding proteins - used to develop transgenic plants which can have enhanced or decreased sucrose uptake activity in developing seeds
PS	PT Claim 7; Pag 39-40; 58pp; English.
CC	This sequence represents a novel sucrose binding protein, SBP2 isolated
RESULT	7
ID	W31853 standard; Protein; 898 AA.
AC	W31853;
DT	27-APR-1998 (first entry)
PT	Mycobacterium tuberculosis 77 kDa protein.
KW	tuberculosis; mycobacteria; infection; diagnosis;
CC	anti-mycobacterial; antibiotic; vaccine.
OS	Mycobacterium tuberculosis.
DR	W09741152-A2.
PN	06-NOV-1997.
PF	18-APR-1997; E01973.
PR	29-APR-1996; DE-017184.
PA	(GBFRB) GBF GES BIOTEC FORSCHUNG GMBH.
PI	Espitia C, Honisch C, Moreno C, Singh M;
CC	WPI; 97-54975050.
DR	N-PSD8; T93610.
PT	New DNA and related proteins or RNA derived from <i>M. tuberculosis</i> - used for diagnosis of mycobacterial infections, monitoring vaccination and development of anti-mycobacterial agents
PS	Claim 7; Fig 14; 55pp; English.
CC	This novel 77 kDa protein is encoded by an open reading frame of a Mycobacterium tuberculosis DNA fragment (see T93610) containing polymorphic GC-rich sequences. It is highly enriched in glycine and may be a cell wall protein. Novel <i>M. tuberculosis</i> proteins (see WO971851-57) are claimed. These can be produced as recombinant proteins, especially in bacterial, yeast, fungal or higher eukaryotic host cells, and used for diagnosing tuberculosis and other mycobacterial infections in humans or animals. The claimed proteins can also be used for epidemiological studies, for monitoring vaccination, and for the development of vaccines and anti-mycobacterial drugs.
SQ	Sequence 898 AA;
Query Match	22.4%; Score 95; DB 1; Length 409;
Best Local Similarity	36.2%; Pred. No. 1.24e+00;
Matches	17; Conservative 11; Mismatches 13; Indels 6; Gaps 5;
ID	W90341 standard; protein; 489 AA.
AC	W90341;
DT	24-MAY-1999 (first entry)
DE	G. max SBP2 protein.
KW	SBP1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant; seed; carbohydrate content; soybean.
OS	Glycine max.
DR	W09850986-A1.
PN	26-NOV-1998.
PF	21-MAY-1998; U10465.
PR	(UNIW ) UNIV WASHINGTON STATE RES FOUND.
PA	PAI Chao WS, Grimes HD;
PI	WPI; 99-070155/06.
DR	New modified plant sucrose binding proteins - used to develop transgenic plants which can have enhanced or decreased sucrose uptake activity in developing seeds
PT	PT Claim 13b; Page 37-38; 58pp; English.
PS	This sequence represents a novel sucrose binding protein, SBP2 isolated from Glycine max. This protein is used in a method resulting in the production of a modified plant sucrose binding protein (SBP) which has a modified amino acid sequence compared to a corresponding wild-type SBP, and where expression of the modified SBP in a yeast assay system confers enhanced sucrose uptake compared to the corresponding wild-type SBP. The products of the invention can be used for producing transgenic plants which have modified sucrose uptake activity, particularly in developing seeds. Enhanced sucrose uptake activity in developing seeds may be desirable where it is an advantage to increase the carbohydrate content of the seed (e.g. where the seed is the primary plant material harvested, such as soybean). In contrast, decreased sucrose uptake activity in seeds might be desirable where the vegetative material of the plant is harvested. The SBP regulatory regions confer specific or enhanced expression in developing seeds and so may be used to express any transgene in developing seeds.
SQ	Sequence 489 AA;
Query Match	22.4%; Score 95; DB 1; Length 489;
Best Local Similarity	36.2%; Pred. No. 1.24e+00;
Matches	17; Conservative 11; Mismatches 13; Indels 6; Gaps 5;
ID	39 LYTCKKDQCDR-QYEDSKRCLQC-DSMK-E-PEKQVETEERK 82
AC	41 ILOOCVQRCPYRSHA-R-CVQBCRDQQGHRHEQEBOGR 84
DT	26-NOV-1998.
PT	New modified plant sucrose binding proteins - used to develop transgenic plants which can have enhanced or decreased sucrose uptake activity in developing seeds
PS	PT Claim 7; Pag 39-40; 58pp; English.
CC	This sequence represents a novel sucrose binding protein, SBP2 isolated

**Query Match** 20.9%; Score 89; DB 1; Length 525;  
**Best Local Similarity** 28.9%; Pred. No. 3.82e+00; **Matches** 11; **Conservative** 14; **Mismatches** 12; **Indels** 1; **Gaps** 1;

**Db** 86 QQCQCRQCQEQQQGPRQQCQORKCWEQYKEQEREEHEN 123  
**Oy** 42 QQCVRQR-QEPRTYSHARCVQECRDDQQQHGRHQEE 78

**RESULT** 11

**ID** R20181 standard; **Protein**; 566 AA.

**AC** R20181; DR-1992 (first entry)

**CC** Sequence encoded by 67 kD T. cacao protein cDNA.

**DE** Sequence encoded by 67 kD T. cacao protein cDNA.

**KW** Cacao; flavour; vicilin; seed storage protein.

**OS** Theobroma cacao.

**PI** WO9119801-A.

**PD** 26-DEC-1991.

**PF** 07-JUN-1991; G00914; 11-JUN-1990; GB-01016.

**PP** (MRSC ) MARS UK LTD.

**PT** Spencer ME, Rodge R, Deakin EA, Ashton S;

**DR** WPI: 92-024418-03.

**N-PSDB**; Q20377.

**RECOMBINANT COCOA PROTEINS - are responsible for flavour in cocoa beans and produced in large quantities using yeast and bacterial expression vectors**

**PT** Claim 4; Fig 2; 59pp; English.

The inventors claim a 67 kD and 31 kD T. cacao protein, and fragments, and encoding DNAs. The 47 kD and 31 kD proteins are derived from the 67 kD precursor. T. cacao protein cDNA was detected in a cDNA library prepared from immature cocoa beans RNA using a probe based on the AA sequence of a CNBr peptide common to the 47 kD and 31 kD polypeptides. Homology searches revealed close homologies between the 67 kD polypeptide and the vicilins, which are seed storage proteins.

**Sequence** 566 AA:

**Query Match** 20.9%; Score 89; DB 1; Length 566;  
**Best Local Similarity** 28.9%; Pred. No. 3.82e+00; **Matches** 11; **Conservative** 14; **Mismatches** 12; **Indels** 1; **Gaps** 1;

**Db** 86 QQCQCRQCQEQQQGPRQQCQORKCWEQYKEQEREEHEN 123  
**Oy** 42 QQCVRQR-QEPRTYSHARCVQECRDDQQQHGRHQEE 78

**RESULT** 13

**ID** W55348 standard; **protein**; 97 AA.

**AC** W55348; DR-1998 (first entry)

**CC** Human Erbb2 extracellular domain protein fragment (aa 529-625).

**DE** Human Erbb2 extracellular domain protein fragment (aa 529-625). Erbb2; epitope; monoclonal antibody; identification; apoptosis; detection; treatment; disorder; tumour; benign; malignant; leukaemia; lymphoid malignancy; inflammation; angiogenic; immunological.

**KW** Homo sapiens.

**OS** WO8117197-A1.

**PI** Fendly BM, Phillips GD, Scheuermann RH, Uhr JW;

**DR** W8-261493/23.

**PT** New anti-ErbB2 antibodies - which induce apoptosis in cells which overexpress Erbb2, used to treat e.g. tumours or inflammatory disorders; Page 46; 72pp; English.

**CC** This sequence represents a fragment of the human Erbb2 extracellular domain corresponding to amino acids 529-625 which is capable of binding

**Query Match** 20.0%; Score 85; DB 1; Length 450;  
**Best Local Similarity** 33.3%; Pred. No. 8.02e+00; **Matches** 13; **Conservative** 13; **Mismatches** 10; **Indels** 3; **Gaps** 3;

**Db** 398 QPDRGREHQ-RCRESEDETERERERHRRQESERARG 435  
**Oy** 49 RQEPRTYSHARCVQECRDDQQQHGRHQEE 85

**RESULT** 13

**ID** W55348 standard; **protein**; 97 AA.

**AC** W55348; DR-1998 (first entry)

**CC** Human Erbb2 extracellular domain protein fragment (aa 529-625). Erbb2; epitope; monoclonal antibody; identification; apoptosis; detection; treatment; disorder; tumour; benign; malignant; leukaemia; lymphoid malignancy; inflammation; angiogenic; immunological.

**DE** (GENETECH INC. (TEXA ) UNIV TEXAS SYSTEM.

**PI** Fendly BM, Phillips GD, Scheuermann RH, Uhr JW;

**DR** W46506; DR-1998 (first entry)

**PT** Tyrosine kinase associated protein 1.

**CC** Tyrosine kinase associated protein-1; TKA-1; antibody; tyrosine kinase associated protein; receptor dimerisation; Homo sapiens.

**OS** Theobroma cacao.

**PI** WO927805-A1.

**PD** 02-JUL-1998.

**PF** 22-DEC-1997; AU0874.

**PR** 20-DEC-1996; AU-004175.

**PA** (RETR) COOP RES CENT TROPICAL PLANT PATHOLOGY.

**PI** Bower NI, Coulter KC, Green JI, Manners JM, Marcus JP;

**DR** WPI: 98-3729-32.

**PT** Novel anti-microbial protein from e.g. Macadamia integrifolia - useful for controlling microbial infestations of plants or mammals

**PR** Claim 1; Page 47-49; 96pp; English.

**PS** The sequence is that of an antimicrobial protein which can be used to control microbial infestations in plants and mammalian animals.

**SQ** Sequence 525 AA;

**Query Match** 20.9%; Score 89; DB 1; Length 525;  
**Best Local Similarity** 28.9%; Pred. No. 3.82e+00; **Matches** 11; **Conservative** 14; **Mismatches** 12; **Indels** 1; **Gaps** 1;

**Db** 86 QQCQCRQCQEQQQGPRQQCQORKCWEQYKEQEREEHEN 123  
**Oy** 42 QQCVRQR-QEPRTYSHARCVQECRDDQQQHGRHQEE 78

**RESULT** 11

**ID** R20181 standard; **Protein**; 566 AA.

**AC** R20181; DR-1992 (first entry)

**CC** Sequence encoded by 67 kD T. cacao protein cDNA.

**DE** Sequence encoded by 67 kD T. cacao protein cDNA.

**KW** Tyrosine kinase associated protein-1; TKA-1; antibody; tyrosine kinase associated protein; receptor dimerisation; Homo sapiens.

**OS** Theobroma cacao.

**PI** WO927805-A1.

**PD** 02-JUL-1998.

**PF** 16-OCT-1996; U16510.

**PR** 13-JUN-1996; US-666067.

**PA** (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

**PI** Seedorf L, Ulrich A;

**DR** WPI: 98-101049/09.

**PT** Tyrosine Kinase associated protein-1 - used for the diagnosis and treatment of TKA-1 related diseases

**PS** Claim 2; Fig 1; 61pp; English.

**CC** The Tyrosine Kinase associated protein-1 (TKA-1) contains a stretch of 106 amino acids (aa1-112) which is duplicated within the sequence (aa 146-252) with 65% identity, and again (aa336-475) with 47% identity. A binding agent of TKA-1, able to bind to a TKA-1 polypeptide, or the full length TKA-1 protein can both be used in a method for disrupting or promoting receptor dimerisation. They can also be used to identify agents capable of interfering with the interaction between them. The TKA-1 antibody can be used for the detection of TKA-1. The TKA-1 protein, antibody and binding agent can all be used in the diagnosis and treatment of TKA-1 related diseases and conditions.

**SQ** Sequence 450 AA;

**Query Match** 20.0%; Score 85; DB 1; Length 450;  
**Best Local Similarity** 33.3%; Pred. No. 8.02e+00; **Matches** 13; **Conservative** 13; **Mismatches** 10; **Indels** 3; **Gaps** 3;

**Db** 398 QPDRGREHQ-RCRESEDETERERERHRRQESERARG 435  
**Oy** 49 RQEPRTYSHARCVQECRDDQQQHGRHQEE 85

**RESULT** 13

**ID** W55348 standard; **protein**; 97 AA.

**AC** W55348; DR-1998 (first entry)

**CC** Human Erbb2 extracellular domain protein fragment (aa 529-625). Erbb2; epitope; monoclonal antibody; identification; apoptosis; detection; treatment; disorder; tumour; benign; malignant; leukaemia; lymphoid malignancy; inflammation; angiogenic; immunological.

**DE** (GENETECH INC. (TEXA ) UNIV TEXAS SYSTEM.

**PI** Fendly BM, Phillips GD, Scheuermann RH, Uhr JW;

**DR** W46506; DR-1998 (first entry)

**PT** Tyrosine kinase associated protein 1.

**CC** Tyrosine kinase associated protein 1.

**OS** Theobroma cacao.

**PI** WO927805-A1.

**PD** 02-JUL-1998.

**PF** 09-OCT-1998; U18385.

**PR** 18-OCT-1996; US-31794.

**PA** (GENETECH INC. (TEXA ) UNIV TEXAS SYSTEM.

**PI** Fendly BM, Phillips GD, Scheuermann RH, Uhr JW;

**DR** W8-261493/23.

**PT** New anti-ErbB2 antibodies - which induce apoptosis in cells which overexpress Erbb2, used to treat e.g. tumours or inflammatory disorders; Page 46; 72pp; English.

**CC** This sequence represents a fragment of the human Erbb2 extracellular domain corresponding to amino acids 529-625 which is capable of binding

CC monoclonal antibodies 4D5. This region is used in a method which  
 CC identifies antibodies capable of binding to Erbb2 and induce apoptosis of  
 CC a cell which overexpresses Erbb2. The antibodies can also be used to  
 detect Erbb2 on a cell. The antibodies can be used for treating disorders  
 such as benign or malignant tumours, (e.g. renal, liver, kidney, bladder,  
 CC breast, gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval,  
 CC thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head  
 and neck tumours), leukaemia's, lymphoid malignancies, other disorders  
 such as neuronal, glial, astrocytal, hypothalamic and other glandular,  
 CC macrophagal, epithelial, stromal and blactoocelial disorders, and  
 CC inflammatory, angiogenic and immunologic disorders.

SQ Sequence 97 AA;

Query Match 19.8%; Score 84; DB 1; Length 97;  
 Best Local Similarity 44.4%; Pred. No. 9.64e+00; Mismatches 7; Indels 6; Gaps 5;  
 Matches 16; Conservative 7; Mismatches 7; Indels 6; Gaps 5;

Db 10 QBCVEECRVLQGPREVNARICLCP-CHPECOPQNG 44  
 QY' 42 QQCVRQR-QERPR-YSHAR-CVQECRDD-QQQHG 72

RESULT 14

ID W90340 standard; protein; 444 AA.  
 AC W90340;  
 DT 24-MAY-1999 (first entry)  
 DE G. max truncated SBP1 protein.

DB SPB1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant;  
 CC seed; carbohydrate content; soybean.  
 CC Glycine max.

PR (UNIW ) UNIV WASHINGTON STATE RES FOUND.  
 PI Chao WS, Grimes HD;  
 PT WPI; 99-070155/06.  
 PA (UNIW ) UNIV WASHINGTON STATE RES FOUND.  
 DR 22-MAY-1997; US-047558.

PP 21-MAY-1998; U10465;  
 PR 26-NOV-1998; U10465.  
 DE G. max truncated SBP1 protein.

PT SPB1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant;  
 CC seed; carbohydrate content; soybean.  
 CC Glycine max.

PS WO95086-A1.  
 PD 26 NOV-1998.  
 PR 22-MAY-1999; US-047558.

PT SPB1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant;  
 CC seed; carbohydrate content; soybean.  
 CC Glycine max.

PR (UNIW ) UNIV WASHINGTON STATE RES FOUND.  
 PI Chao WS, Grimes HD;

PT WPI; 99-070155/06.

This sequence represents a novel sucrose binding protein, SBP1 isolated  
 from Glycine max. This protein is used in a method resulting in the  
 production of a modified plant sucrose binding protein (SBP) which has a  
 modified amino acid sequence compared to a corresponding wild-type SBP,  
 and where expression of the modified SBP in a yeast assay system confers  
 enhanced sucrose uptake compared to the corresponding wild-type SBP.

The products of the invention can be used for producing transgenic plants  
 which have modified sucrose uptake activity, particularly in developing  
 seeds. Enhanced sucrose uptake activity in developing seeds may be  
 desirable where it is an advantage to increase the carbohydrate content  
 of the seed (e.g. where the seed is the primary plant material harvested,  
 such as soybean). In contrast, decreased sucrose uptake activity in  
 seeds might be desirable where the vegetative material of the plant is  
 harvested. The SBP regulatory regions confer specific or enhanced  
 expression in developing seeds and so may be used to express any  
 CC transgene in developing seeds.

SQ Sequence 524 AA;

Query Match 19.8%; Score 84; DB 1; Length 524;  
 Best Local Similarity 29.2%; Pred. No. 9.64e+00; Mismatches 14; Indels 5; Gaps 4;  
 Matches 14; Conservative 14; Mismatches 15; Indels 5; Gaps 4;

Db 40 LVTCKHQOCQQQ-QYTEDGDKRVCLQSCDRYHMKREKQEQETREK 86  
 QY' 41 LQQCVRQRCPRPRYSHA--R-CVQEC-RDDQQHGRHEOEQQGR 84

Search completed: Sat May 13 09:00:01 2000  
 Job time : 8 secs.

SQ Sequence 524 AA;

Query Match 19.8%; Score 84; DB 1; Length 444;  
 Best Local Similarity 29.2%; Pred. No. 9.64e+00; Mismatches 15; Indels 5; Gaps 4;

Matches 14; Conservative 14; Mismatches 15; Indels 5; Gaps 4;

Db 40 LVTCKHQOCQQQ-QYTEDGDKRVCLQSCDRYHMKREKQEQETREK 86  
 QY' 41 LQQCVRQRCPRPRYSHA--R-CVQEC-RDDQQHGRHEOEQQGR 84

RESULT 15  
 ID W90339 standard; protein; 524 AA.  
 AC W90339;  
 DT 24-MAY-1999 (first entry)  
 DE G. max SBP1 protein.

